

RAW SEQUENCE LISTING

DATE: 04/26/2001

PATENT APPLICATION: US/09/308,435A

TIME: 11:52:03

Input Set : A:\Astra561.app

Output Set: N:\CRF3\04262001\I308435A.raw

Does Not Comply
Corrected Diskette NeededP.6

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3 <110> APPLICANT: Astra Aktiebolag
5 <120> TITLE OF INVENTION: Vaccine Delivery System and Method of Production
7 <130> FILE REFERENCE: 1103326-0560
9 <140> CURRENT APPLICATION NUMBER: 09/308,435A
10 <141> CURRENT FILING DATE: 1999-05-19
12 <150> PRIOR APPLICATION NUMBER: PCT/SE99/00582
13 <151> PRIOR FILING DATE: 1999-04-09
15 <150> PRIOR APPLICATION NUMBER: SE 9801288-3
16 <151> PRIOR FILING DATE: 1998-04-14
18 <160> NUMBER OF SEQ ID NOS: 25
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1670
24 <212> TYPE: DNA
25 <213> ORGANISM: Helicobacter pylori
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28 <221> NAME/KEY: CDS
29 <222> LOCATION: (793)..(1572)
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36 gatttgattt tagggaatta catgcaagtg aatgaaaaaa acattcaagc gtttgccccc 180
38 aaacaataag gtaaaaaatg ccactcactc atttgaatga agaaaatcaa cctaaaatgg 240
40 tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggg cgtatcagca 300
42 tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggg ccggtattac 360
44 aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420
46 gccatccaat catgctcaat ggggtggata ttgatatttt agaagaaaaa gagacttgta 480
48 gttttaaact ctatgcgaga gtcaaaactc aagctaaaac gggcgtagaa atggaagcgc 540
50 taatgagtgt gagcgtaggg cttttaacca tttatgacat ggtgaaagcc attgataaga 600
52 gcatgacaat tagcgggtgtg atgctggaat ataaaagtgg aggcaaaagt ggggattata 660
54 acgctaaaaa atagaaaaag actgataatc taaagatatt agggtaaaat aacattttga 720
56 caacaaaagc gtgttggttg cttcggattt gttgttatag aagtctaaaa tattacaatc 780
58 aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831
59           Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys
60           1           5           10
62 aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879
63 Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser
64           15           20           25
66 ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927
67 Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His
68           30           35           40           45
70 cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975
71 Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu
72           50           55           60
74 agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac 1023
75 Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn
76           65           70           75

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78 aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat 1071
79 Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn
80      80      85      90
82 caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt 1119
83 Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe
84      95      100      105
86 tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc 1167
87 Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly
88 110      115      120      125
90 gaa att gtt tta cgc ccc gat cct aaa agg acc ata cag aaa aaa tca 1215
91 Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser
92      130      135      140
94 gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt 1263
95 Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val
96      145      150      155
98 tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt 1311
99 Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser
100      160      165      170
102 ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att 1359
103 Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile
104      175      180      185
106 caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta 1407
107 Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu
108 190      195      200      205
110 gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag 1455
111 Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys
112      210      215      220
114 agc gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa 1503
115 Ser Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys
116      225      230      235
118 aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa 1551
119 Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu
120      240      245      250
122 tta aaa ggc aaa aga aac cga taaaaacaaa taacgcataa gaaaagaacg 1602
123 Leu Lys Gly Lys Arg Asn Arg
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128 tgatgac 1670
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132 <211> LENGTH: 260
133 <212> TYPE: PRT
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138 1 5 10 15
140 Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser Pro His Ile
141 20 25 30
143 Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
144 35 40 45

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146 Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu Arg Pro Ala
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149 Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
150 65                      70                      75                      80
152 Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
153                      85                      90                      95
155 Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
156                      100                     105                     110
158 Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
159                      115                     120                     125
161 Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
162      130                      135                      140
164 Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
165 145                      150                      155                      160
167 Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
168                      165                      170                      175
170 Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
171                      180                      185                      190
173 Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
174                      195                     200                     205
176 Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu
177      210                      215                      220
179 Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
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193 <213> ORGANISM: Helicobacter pylori
195 <220> FEATURE:
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204 gatttgattt tagggaatta catgcaagtg aatgaaaaaa acattcaagc gtttgccccc 180
206 aaacaataag gtaaaaaatg ccactcactc atttgaatga agaaaatcaa cctaaaatgg 240
208 tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggg cgtatcagca 300
210 tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggt ccggtattac 360
212 aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420
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226 aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831
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230 aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879
231 Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser
232           15           20           25
234 ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927
235 Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His
236           30           35           40           45
238 cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975
239 Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu
240           50           55           60
242 agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac 1023
243 Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn
244           65           70           75
246 aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat 1071
247 Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn
248           80           85           90
250 caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt 1119
251 Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe
252           95           100           105
254 tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc 1167
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264           145           150           155
266 tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt 1311
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268           160           165           170
270 ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att 1359
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272           175           180           185
274 caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta 1407
275 Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu
276           190           195           200           205
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280           210           215           220
282 aga gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa 1503
283 Arg Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys
284           225           230           235
286 aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa 1551
287 Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu
288           240           245           250
290 tta aaa ggc aaa aga aac cga taaaaacaaa taacgcataa gaaaagaacg 1602

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291 Leu Lys Gly Lys Arg Asn Arg
292      255      260
294 cttgaataaaa ctgcttaaaaa aggggtttttt agcggttcttt ttgagcgtgt atttaagggc 1662
296 tgatgatac                                     1670
299 <210> SEQ ID NO: 4
300 <211> LENGTH: 260
301 <212> TYPE: PRT
302 <213> ORGANISM: Helicobacter pylori
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311 Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
312      35      40      45
314 Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Arg Pro Ala
315      50      55      60
317 Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
318   65      70      75      80
320 Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
321      85      90      95
323 Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
324      100     105     110
326 Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
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329 Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
330      130     135     140
332 Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
333   145     150     155     160
335 Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
336      165     170     175
338 Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
339      180     185     190
341 Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
342      195     200     205
344 Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Arg Ala Leu
345      210     215     220
347 Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
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09/28, 435A 6

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response needed

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where are amino acids?

VERIFICATION SUMMARY

DATE: 04/26/2001

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Input Set : A:\Astra561.app

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